

RAW SEQUENCE LISTING

DATE: 05/27/2001

PATENT APPLICATION: US/09/847,208

TIME: 16:48:07

Input Set : A:\Pto.amc

Output Set: C:\CRF3\05272001\I847208.raw

3 <110> APPLICANT: Saxon, Andrew
4 Zhang, Ke
5 Zhu, Daocheng
7 <120> TITLE OF INVENTION: FUSION MOLECULES AND TREATMENT OF
8 IgE-MEDIATED ALLERGIC DISEASES
10 <130> FILE REFERENCE: UC67.002A
C--> 12 <140> CURRENT APPLICATION NUMBER: US/09/847,208
C--> 12 <141> CURRENT FILING DATE: 2001-05-01
12 <160> NUMBER OF SEQ ID NOS: 177
14 <170> SOFTWARE: FastSEQ for Windows Version 4.0
16 <210> SEQ ID NO: 1
17 <211> LENGTH: 696
18 <212> TYPE: DNA
19 <213> ORGANISM: Homo sapiens
21 <400> SEQUENCE: 1
22 gagcccaaat cttgtgacaa aactcacaca tgcccaccgt gccagcacc tgaactcctg 60
23 gggggaccgt cagtcttcct cttcccccca aaaccaag acaccctcat gatctcccgg 120
24 acccctgagg tcacatgcgt ggtggtggac gtgagccacg aagaccctga ggtcaagttc 180
25 aactggtacg tggacggcgt ggaggtgcat aatgttaaga caaagccgcg ggaggagcag 240
26 tacaacagca cgtaccgtgt ggtcagcgtc ctcaccgtcc tgcaccagaa ctggatgaat 300
27 ggaaaggagt acaagtgcaa ggtctccaac aaagccctcc cagcccccat cgagaaaacc 360
28 atctccaaag ccaaagtga gccccgagaa ccacaggtgt acaccctgcc cccatcccgg 420
29 gatgagctga ccaagaacca ggtcagcctg acctgcctgg tcaaaggctt ctatcccagc 480
30 gacatcgccg tggagtggga gagcaatggg cagccggaga acaactacaa gaccacgcct 540
31 cccgtgctgg actccgtcgg ctccttcttc ctctacagca agctcaccgt ggacaagagc 600
32 aggtggcagc aggggaacgt cttctcatgc tccgtgatgc atgaggctct gcacaaccac 660
33 taccagcaga ggagcctctc cctgtctccg ggtaaa 696
35 <210> SEQ ID NO: 2
36 <211> LENGTH: 330
37 <212> TYPE: PRT
38 <213> ORGANISM: Homo sapiens
40 <400> SEQUENCE: 2
41 Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu Ala Pro Ser Ser Lys
42 1 5 10 15
43 Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr
44 20 25 30
45 Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser
46 35 40 45
47 Gly Val His Thr Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser
48 50 55 60
49 Leu Ser Ser Val Val Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr
50 65 70 75 80
51 Tyr Ile Cys Asn Val Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys
52 85 90 95
53 Lys Val Glu Pro Lys Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys
54 100 105 110
55 Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro

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56          115          120          125
57 Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys
58          130          135          140
59 Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp
60 145          150          155          160
61 Tyr Val Asp Gly Val Glu Val His Asn Val Lys Thr Lys Pro Arg Glu
62          165          170          175
63 Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu
64          180          185          190
65 His Gln Asn Trp Met Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn
66          195          200          205
67 Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Val
68          210          215          220
69 Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu
70 225          230          235          240
71 Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr
72          245          250          255
73 Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn
74          260          265          270
75 Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Val Gly Ser Phe Phe
76          275          280          285
77 Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn
78          290          295          300
79 Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Gln
80 305          310          315          320
81 Gln Arg Ser Leu Ser Leu Ser Pro Gly Lys
82          325          330
85 <210> SEQ ID NO: 3
86 <211> LENGTH: 232
87 <212> TYPE: PRT
88 <213> ORGANISM: Homo sapiens
90 <400> SEQUENCE: 3
91 Glu Pro Lys Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala
92 1          5          10          15
93 Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro
94          20          25          30
95 Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val
96          35          40          45
97 Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val
98          50          55          60
99 Asp Gly Val Glu Val His Asn Val Lys Thr Lys Pro Arg Glu Glu Gln
100 65          70          75          80
101 Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln
102          85          90          95
103 Asn Trp Met Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala
104          100          105          110
105 Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Val Gln Pro
106          115          120          125
107 Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr

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```

108      130      135      140
109 Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser
110 145      150      155      160
111 Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr
112      165      170      175
113 Lys Thr Thr Pro Pro Val Leu Asp Ser Val Gly Ser Phe Phe Leu Tyr
114      180      185      190
115 Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe
116      195      200      205
117 Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Gln Gln Arg
118      210      215      220
119 Ser Leu Ser Leu Ser Pro Gly Lys
120 225      230
123 <210> SEQ ID NO: 4
124 <211> LENGTH: 1445
125 <212> TYPE: DNA
126 <213> ORGANISM: Homo sapiens
128 <400> SEQUENCE: 4
129 tccacacaga gccatccgt ctcccccttg acccgctgct gcaaaaacat tccctccaat 60
130 gccacctccg tgactctggg ctgacctggc acgggtact tcccggagcc ggtgatggtg 120
131 acctgggaca caggtccct caacgggaca actatgacct taccagccac caccctcacg 180
132 ctctctggtc actatgccac catcagcttg ctgaccgtct cgggtgctg ggccaagcag 240
133 atgttcacct gccgtgtggc acacactcca tgcgccacag actgggtcga caacaaacc 300
134 ttcagcgtct gctccaggga cttacccccg ccacccgtga agatcttaca gtcgtcctgc 360
135 gacggcgcg ggcacttccc cccgaccatc cagctcctgt gcctcgtctc tgggtacacc 420
136 ccagggaacta tcaacatcac ctggctggag gacgggcagg tcatggacgt ggacttgtcc 480
137 accgcctcta ccacgcagga gggtagctg gcctccacac aaagcgagct caccctcagc 540
138 cagaagcact ggctgtcaga ccgcacctac acctgccagg tcacctatca aggtcacacc 600
139 tttgaggaca gcaccaagaa gtgtgcagat tccaaccga gaggggtgag cgcctaccta 660
140 agccggccca gcccggttca cctgttcac cgcaagtcgc ccacgatcac ctgtctggtg 720
141 gtggacctgg caccagcaa ggggaccgtg aacctgacct ggtcccgggc cagtgggaag 780
142 cctgtgaacc actccaccag aaaggaggag aagcagcgca atggcacgtt aaccgtcacg 840
143 tccaccctgc cgggtggcac ccgagactgg atcgagggg agacctacca gtgcagggtg 900
144 accaccccc acctgcccag ggccctcatg cggtcacga ccaagaccag cggcccgcgt 960
145 gctgccccgg aagtctatgc gtttgcgac ccggagtggc cggggagccg ggacaagcgc 1020
146 accctgcct gctgatecca gaattcatg cctgaggaca tctcggtgca gtggctgcac 1080
147 aacgaggtgc agtcccga cgccggcac agcacgacgc agccccgaa gaccaagggc 1140
148 tccggcttct tctcttcag ccgcctggag gtgaccagg ccgaatggga gcagaaagat 1200
149 gattcatct gccgtgcagt ccataggga gcgagccct cacagaccgt ccagcgagcg 1260
150 gtgtctgtaa atcccggtaa atgacgtact cctgcctccc tccctcccag ggtccatcc 1320
151 agctgtgcag tggggaggac tggccagacc ttctgtccac tgttgcaatg accccaggaa 1380
152 gctaccccca ataaactgtg cctgctcaga gccccagtac acccattctt gggagcgggc 1440
153 agggc
155 <210> SEQ ID NO: 5
156 <211> LENGTH: 427
157 <212> TYPE: PRT
158 <213> ORGANISM: Homo sapiens
160 <400> SEQUENCE: 5
161 Ser Thr Gln Ser Pro Ser Val Phe Pro Leu Thr Arg Cys Cys Lys Asn

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```

162 1 5 10 15
163 Ile Pro Ser Asn Ala Thr Ser Val Thr Leu Gly Cys Leu Ala Thr Gly
164 20 25 30
165 Tyr Phe Pro Glu Pro Val Met Val Thr Trp Asp Thr Gly Ser Leu Asn
166 35 40 45
167 Gly Thr Thr Met Thr Leu Pro Ala Thr Thr Leu Thr Leu Ser Gly His
168 50 55 60
169 Tyr Ala Thr Ile Ser Leu Leu Thr Val Ser Gly Ala Trp Ala Lys Gln
170 65 70 75 80
171 Met Phe Thr Cys Arg Val Ala His Thr Pro Ser Ser Thr Asp Trp Val
172 85 90 95
173 Asp Asn Lys Thr Phe Ser Val Cys Ser Arg Asp Phe Thr Pro Pro Thr
174 100 105 110
175 Val Lys Ile Leu Gln Ser Ser Cys Asp Gly Gly Gly His Phe Pro Pro
176 115 120 125
177 Thr Ile Gln Leu Leu Cys Leu Val Ser Gly Tyr Thr Pro Gly Thr Ile
178 130 135 140
179 Asn Ile Thr Trp Leu Glu Asp Gly Gln Val Met Asp Val Asp Leu Ser
180 145 150 155 160
181 Thr Ala Ser Thr Thr Gln Glu Gly Glu Leu Ala Ser Thr Gln Ser Glu
182 165 170 175
183 Leu Thr Leu Ser Gln Lys His Trp Leu Ser Asp Arg Thr Tyr Thr Cys
184 180 185 190
185 Gln Val Thr Tyr Gln Gly His Thr Phe Glu Asp Ser Thr Lys Lys Cys
186 195 200 205
187 Ala Asp Ser Asn Pro Arg Gly Val Ser Ala Tyr Leu Ser Arg Pro Ser
188 210 215 220
189 Pro Phe Asp Leu Phe Ile Arg Lys Ser Pro Thr Ile Thr Cys Leu Val
190 225 230 235 240
191 Val Asp Leu Ala Pro Ser Lys Gly Thr Val Asn Leu Thr Trp Ser Arg
192 245 250 255
193 Ala Ser Gly Lys Pro Val Asn His Ser Thr Arg Lys Glu Glu Lys Gln
194 260 265 270
195 Arg Asn Gly Thr Leu Thr Val Thr Ser Thr Leu Pro Val Gly Thr Arg
196 275 280 285
197 Asp Trp Ile Glu Gly Glu Thr Tyr Gln Cys Arg Val Thr His Pro His
198 290 295 300
199 Leu Pro Arg Ala Leu Met Arg Ser Thr Thr Lys Thr Ser Gly Pro Arg
200 305 310 315 320
201 Ala Ala Pro Glu Val Tyr Ala Phe Ala Thr Pro Glu Trp Pro Gly Ser
202 325 330 335
203 Arg Asp Lys Arg Thr Leu Ala Cys Leu Ile Gln Asn Phe Met Pro Glu
204 340 345 350
205 Asp Ile Ser Val Gln Trp Leu His Asn Glu Val Gln Leu Pro Asp Ala
206 355 360 365
207 Arg His Ser Thr Thr Gln Pro Arg Lys Thr Lys Gly Ser Gly Phe Phe
208 370 375 380
209 Val Phe Ser Arg Leu Glu Val Thr Arg Ala Glu Trp Glu Gln Lys Asp
210 385 390 395 400

```

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```

211 Glu Phe Ile Cys Arg Ala Val His Glu Ala Ala Ser Pro Ser Gln Thr
212                               405                               410                               415
213 Val Gln Arg Ala Val Ser Val Asn Pro Gly Lys
214                               420                               425
217 <210> SEQ ID NO: 6
218 <211> LENGTH: 320
219 <212> TYPE: PRT
220 <213> ORGANISM: Homo sapiens
222 <400> SEQUENCE: 6
223 Phe Thr Pro Pro Thr Val Lys Ile Leu Gln Ser Ser Cys Asp Gly Gly
224 1                               5                               10                               15
225 Gly His Phe Pro Pro Thr Ile Gln Leu Leu Cys Leu Val Ser Gly Tyr
226                               20                               25                               30
227 Thr Pro Gly Thr Ile Asn Ile Thr Trp Leu Glu Asp Gly Gln Val Met
228                               35                               40                               45
229 Asp Val Asp Leu Ser Thr Ala Ser Thr Thr Gln Glu Gly Glu Leu Ala
230 50                               55                               60
231 Ser Thr Gln Ser Glu Leu Thr Leu Ser Gln Lys His Trp Leu Ser Asp
232 65                               70                               75                               80
233 Arg Thr Tyr Thr Cys Gln Val Thr Tyr Gln Gly His Thr Phe Glu Asp
234                               85                               90                               95
235 Ser Thr Lys Lys Cys Ala Asp Ser Asn Pro Arg Gly Val Ser Ala Tyr
236                               100                              105                              110
237 Leu Ser Arg Pro Ser Pro Phe Asp Leu Phe Ile Arg Lys Ser Pro Thr
238                               115                              120                              125
239 Ile Thr Cys Leu Val Val Asp Leu Ala Pro Ser Lys Gly Thr Val Asn
240 130                              135                              140
241 Leu Thr Trp Ser Arg Ala Ser Gly Lys Pro Val Asn His Ser Thr Arg
242 145                              150                              155                              160
243 Lys Glu Glu Lys Gln Arg Asn Gly Thr Leu Thr Val Thr Ser Thr Leu
244                               165                              170                              175
245 Pro Val Gly Thr Arg Asp Trp Ile Glu Gly Glu Thr Tyr Gln Cys Arg
246                               180                              185                              190
247 Val Thr His Pro His Leu Pro Arg Ala Leu Met Arg Ser Thr Thr Lys
248                               195                              200                              205
249 Thr Ser Gly Pro Arg Ala Ala Pro Glu Val Tyr Ala Phe Ala Thr Pro
250 210                              215                              220
251 Glu Trp Trp Pro Gly Ser Arg Asp Lys Arg Thr Leu Ala Cys Leu Ile Gln
252 225                              230                              235                              240
253 Asn Phe Met Pro Glu Asp Ile Ser Val Gln Trp Leu His Asn Glu Val
254                               245                              250                              255
255 Gln Leu Pro Asp Ala Arg His Ser Thr Thr Gln Pro Arg Lys Thr Lys
256                               260                              265                              270
257 Gly Ser Gly Phe Phe Val Phe Ser Arg Leu Glu Val Thr Arg Ala Glu
258                               275                              280                              285
259 Trp Glu Gln Lys Asp Glu Phe Ile Cys Arg Ala Val His Glu Ala Ala
260 290                              295                              300
261 Ser Pro Ser Gln Thr Val Gln Arg Ala Val Ser Val Asn Pro Gly Lys
262 305                              310                              315                              320

```

Please Note:

Use f n and/ r Xaa hav been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequenc which presents at least one n or Xaa.

file:///C:/CRF3/Outhold/VsrI847208.htm

5/27/01

VERIFICATION SUMMARY

PATENT APPLICATION: US/09/847,208

DATE: 05/27/2001

TIME: 16:48:08

Input Set : A:\Pto.amc

Output Set: C:\CRF3\05272001\I847208.raw

L:12 M:270 C: Current Application Number differs, Replaced Current Application No
L:12 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:3086 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:82
L:3129 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:84
L:3466 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:93
L:3468 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:93
L:3483 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:94
L:4518 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:126
L:6226 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:176
L:6228 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:176
L:6243 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:177
L:6245 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:177